AMENDMENTS

In the Claims:

1. (Currently Amended) A method for detecting whether a subject ~~has~~ is suffering from or is predisposed to developing a disease or condition ~~that is~~ associated with an IL-1 inflammatory haplotype, comprising detecting ~~a plurality of~~ one or more alleles ~~from an IL-1 inflammatory haplotype~~ selected from the group consisting of: ~~an IL-1 44112332 inflammatory haplotype, and an IL-1 33441461 inflammatory haplotype~~ allele 4 of the 222/223 marker of IL-1A, allele 4 of the gz5/gz6 marker of IL-1A, allele 1 of the -889 marker of IL-1A, allele 1 of the +3954 marker of IL-1B, allele 2 of the -511 marker of IL-1B, allele 3 of the gaat.p33330 marker, allele 3 of the Y31 marker, allele 2 of +2018 of IL-1RN, allele 1 of +4845 of IL-1A, allele 3 of the 222/223 marker of IL-1A, allele 3 of the gz5/gz6 marker of IL-1A, allele 2 of the -889 marker of IL-1A, allele 2 of the +3954 marker of IL-1B, allele 1 of the -511 marker of IL-1B, allele 4 of the gaat.p33330 marker, allele 6 of the Y31 marker, allele 1 of +2018 of IL-1RN, allele 2 of +4845 of IL-1A, and allele 1 of the VNTR marker of IL-1RN, wherein the presence of ~~the plurality of~~ said one or more alleles indicates that the subject is predisposed to the development of or has the disease or condition.

2. (Original) A method of claim 1, wherein the disease of condition is selected from the group consisting of an inflammatory disease, a degenerative disease an immunological disorder, an infectious disease, a trauma induced disease, and a cancer.

3. (Original) A method of claim 1, wherein said detecting step is selected from the group consisting of:

   a) allele specific oligonucleotide hybridization;
   b) size analysis;
   c) sequencing;
   d) hybridization;
   e) 5' nuclease digestion;
   f) single-stranded conformation polymorphism;
   g) allele specific hybridization;
   h) primer specific extension; and
   j) oligonucleotide ligation assay.

4. (Original) A method of claim 1, wherein prior to or in conjunction with detection, the nucleic acid sample is subject to an amplification step.

5. (Original) A method of claim 4, wherein said amplification step employs a primer selected from the group consisting of any of SEQ ID Nos.8-32.

6. (Original) A method of claim 3, wherein said size analysis is preceded by a restriction enzyme digestion.

7. (Cancelled)

8. (Currently Amended) A method for selecting an appropriate therapeutic for an individual that ~~has~~ is suffering from or is predisposed to developing a disease or disorder ~~that is~~ associated with an IL-1 polymorphism, comprising the steps of: detecting ~~a plurality of~~ one or more alleles ~~from an IL-1 inflammatory haplotype~~ selected from the group consisting of: ~~an IL-1 44112332 inflammatory haplotype, and an IL-1 33441461 inflammatory haplotype~~ allele 4 of the 222/223 marker of IL-1A, allele 4 of the gz5/gz6 marker of IL-1A, allele 1 of the -889 marker of IL-1A, allele 1 of the +3954 marker of IL-1B, allele 2 of the -511 marker of IL-1B, allele 3 of the gaat.p33330 marker, allele 3 of the Y31 marker, allele 2 of +2018 of IL-1RN, allele 1 of +4845 of IL-1A, allele 3 of the 222/223 marker of IL-1A, allele 3 of the gz5/gz6 marker of IL-1A, allele 2 of the -889 marker of IL-1A, allele 2 of the +3954 marker of IL-1B, allele 1 of the -511 marker of IL-1B, allele 4 of the gaat.p33330 marker, allele 6 of the Y31 marker, allele 1 of +2018 of IL-1RN, allele 2 of +4845 of IL-1A, and allele 1 of the VNTR marker of IL-1RN, and selecting a therapeutic that compensates for a causative functional mutation that is in linkage disequilibrium with the IL-1 alleles.

9. (Original) A method of claim 8, wherein said detecting is performed using a technique selected from the group consisting of:

a) allele specific oligonucleotide hybridization;
b) size analysis;
c) sequencing;
d) hybridization;
e) 5' nuclease digestion;
f) single-stranded conformation polymorphism;
g) allele specific hybridization;
h) primer specific extension; and

j) oligonucleotide ligation assay.

10. (Original) A method of claim 8, wherein prior to or in conjunction with detecting, the nucleic acid sample is subjected to an amplification step.

11. (Original) A method of claim 10, wherein said amplification step employs a primer selected from the group consisting of SEQ ID Nos. 8-32.

12. (Original) A method of claim 9, wherein said size analysis is preceded by a restriction enzyme digestion.

13. (Currently Amended) A method of claim 9, wherein the disease or condition is selected from the group consisting of: an inflammatory disease, a degenerative disease an immunological disorder, an infectious disease, a trauma induced disease, and a cancer.

14. (Original) A method of claim 9, wherein the therapeutic is a modulator of an IL-1 activity.

15. (Original) A method of claim 14, wherein the IL-1 activity is IL-1α.

16. (Original) A method of claim 14, wherein the IL-1 activity is IL-1β.

17. (Original) A method of claim 14, wherein the IL-1 activity is IL-1RN.

18. (Original) A method of claim 14, wherein the modulator of an IL-1 activity is a protein, peptide, peptidomimetic, small molecule, nucleic acid or a nutraceutical.

19. (Original) A method of claim 14, wherein the modulator is an agonist.

20. (Original) A method of claim 14, wherein the modulator is an antagonist.

21. – 28 (Cancelled)

29. (Currently Amended) A method for treating or preventing the development of a disease or condition ~~that is~~ associated with an IL-1 polymorphism in a subject comprising the steps of: detecting ~~a plurality of~~ one or more alleles ~~from an IL-1 inflammatory haplotype~~ selected from the group consisting of: ~~an IL-1 44112332 inflammatory haplotype, and an IL-1 33441461 inflammatory haplotype~~ allele 4 of the 222/223 marker of IL-1A, allele 4 of the gz5/gz6 marker of IL-1A, allele 1 of the -889 marker of IL-1A, allele 1 of the +3954 marker

of IL-1B, allele 2 of the -511 marker of IL-1B, allele 3 of the gaat.p33330 marker, allele 3 of the Y31 marker, allele 2 of +2018 of IL-1RN, allele 1 of +4845 of IL-1A, allele 3 of the 222/223 marker of IL-1A, allele 3 of the gz5/gz6 marker of IL-1A, allele 2 of the -889 marker of IL-1A, allele 2 of the +3954 marker of IL-1B, allele 1 of the -511 marker of IL-1B, allele 4 of the gaat.p33330 marker, allele 6 of the Y31 marker, allele 1 of +2018 of IL-1RN, allele 2 of +4845 of IL-1A, and allele 1 of the VNTR marker of IL-1RN; and administering to the subject a therapeutic that compensates for a causative mutation that is in linkage disequilibrium with the IL-1 inflammatory haplotype.

30. (Original) A method of claim 29, wherein the detecting step is selected from the group consisting of:

a) allele specific oligonucleotide hybridization;
b) size analysis;
c) sequencing;
d) hybridization;
e) 5' nuclease digestion;
f) single-stranded conformation polymorphism;
g) allele specific hybridization;
h) primer specific extension; and
j) oligonucleotide ligation assay.

31. (Original) A method of claim 29, wherein prior to or in conjunction with detecting, the nucleic acid sample is subjected to an amplification step.

32. (Original) A method of claim 29, wherein said amplification step employs a primer selected from the group consisting of any of SEQ ID Nos. 8-32.

33. (Original) A method of claim 30, wherein said size analysis is preceded by a restriction enzyme digestion.

34. (Original) A method of claim 30, wherein the therapeutic is selected from the group consisting of: a modulator of an IL-1 activity.

35. (Original) A method of claim 34, wherein the IL-1 activity is IL-1α.

36. (Original) A method of claim 34, wherein the IL-1 activity is IL-1β.

37. (Original) A method of claim 34, wherein the IL-1 activity is IL-1Ra.

38. (Original) A method of claim 34, wherein the therapeutic is a protein, peptide, peptidomimetic, small molecule or a nucleic acid.

39. (Original) A method of claim 34, wherein the modulator is an agonist.

40. (Original) A method of claim 34, wherein the modulator is an antagonist.

41.– 57. (Cancelled)

58. (New) The method of claim 1, further comprising detecting allele 2 of the VNTR marker of IL-1RN.

59. (New) The method of claim 8, further comprising detecting allele 2 of the VNTR marker of IL-1RN.

60. (New) The method of claim 29, further comprising detecting allele 2 of the VNTR marker of IL-1RN.

61. (New) A method for detecting whether a subject is suffering from or is predisposed to developing a cardiovascular disease, comprising detecting one or more alleles selected from the group consisting of: allele 4 of the 222/223 marker of IL-1A, allele 4 of the gz5/gz6 marker of IL-1A, allele 1 of the -889 marker of IL-1A, allele 1 of the +3954 marker of IL-1B, allele 2 of the -511 marker of IL-1B, allele 3 of the gaat.p33330 marker, allele 3 of the Y31 marker, allele 2 of +2018 of IL-1RN, allele 1 of +4845 of IL-1A, allele 3 of the 222/223 marker of IL-1A, allele 3 of the gz5/gz6 marker of IL-1A, allele 2 of the -889 marker of IL-1A, allele 2 of the +3954 marker of IL-1B, allele 1 of the -511 marker of IL-1B, allele 4 of the gaat.p33330 marker, allele 6 of the Y31 marker, allele 1 of +2018 of IL-1RN, allele 2 of +4845 of IL-1A, and allele 1 of the VNTR marker of IL-1RN, wherein the presence of said one or more alleles indicates that the subject is predisposed to the development of or has a cardiovascular disease.

62. (New) A method for detecting whether a subject is suffering from or is predisposed to developing osteoporosis, comprising detecting one or more alleles selected from the group consisting of: allele 4 of the 222/223 marker of IL-1A, allele 4 of the gz5/gz6 marker of IL-1A, allele 1 of the -889 marker of IL-1A, allele 1 of the +3954 marker of IL-1B, allele 2 of the -511 marker of IL-1B, allele 3 of the gaat.p33330 marker, allele 3 of the Y31 marker,

allele 2 of +2018 of IL-1RN, allele 1 of +4845 of IL-1A, allele 3 of the 222/223 marker of IL-1A, allele 3 of the gz5/gz6 marker of IL-1A, allele 2 of the -889 marker of IL-1A, allele 2 of the +3954 marker of IL-1B, allele 1 of the -511 marker of IL-1B, allele 4 of the gaat.p33330 marker, allele 6 of the Y31 marker, allele 1 of +2018 of IL-1RN, allele 2 of +4845 of IL-1A, and allele 1 of the VNTR marker of IL-1RN, wherein the presence of said one or more alleles indicates that the subject is predisposed to the development of or has osteoporosis.

63. (New) A method for selecting an appropriate therapeutic for an individual that is suffering from or is predisposed to developing a cardiovascular disease, comprising the steps of: detecting one or more alleles selected from the group consisting of: allele 4 of the 222/223 marker of IL-1A, allele 4 of the gz5/gz6 marker of IL-1A, allele 1 of the -889 marker of IL-1A, allele 1 of the +3954 marker of IL-1B, allele 2 of the -511 marker of IL-1B, allele 3 of the gaat.p33330 marker, allele 3 of the Y31 marker, allele 2 of +2018 of IL-1RN, allele 1 of +4845 of IL-1A, allele 3 of the 222/223 marker of IL-1A, allele 3 of the gz5/gz6 marker of IL-1A, allele 2 of the -889 marker of IL-1A, allele 2 of the +3954 marker of IL-1B, allele 1 of the -511 marker of IL-1B, allele 4 of the gaat.p33330 marker, allele 6 of the Y31 marker, allele 1 of +2018 of IL-1RN, allele 2 of +4845 of IL-1A, and allele 1 of the VNTR marker of IL-1RN, and selecting a therapeutic that compensates for a causative functional mutation that is in linkage disequilibrium with the IL-1 alleles.

64. (New) A method for selecting an appropriate therapeutic for an individual that is suffering from or is predisposed to developing osteoporosis, comprising the steps of: detecting one or more alleles selected from the group consisting of: allele 4 of the 222/223 marker of IL-1A, allele 4 of the gz5/gz6 marker of IL-1A, allele 1 of the -889 marker of IL-1A, allele 1 of the +3954 marker of IL-1B, allele 2 of the -511 marker of IL-1B, allele 3 of the gaat.p33330 marker, allele 3 of the Y31 marker, allele 2 of +2018 of IL-1RN, allele 1 of +4845 of IL-1A, allele 3 of the 222/223 marker of IL-1A, allele 3 of the gz5/gz6 marker of IL-1A, allele 2 of the -889 marker of IL-1A, allele 2 of the +3954 marker of IL-1B, allele 1 of the -511 marker of IL-1B, allele 4 of the gaat.p33330 marker, allele 6 of the Y31 marker, allele 1 of +2018 of IL-1RN, allele 2 of +4845 of IL-1A, and allele 1 of the VNTR marker of IL-1RN, and selecting a therapeutic that compensates for a causative functional mutation that is in linkage disequilibrium with the IL-1 alleles.

65. (New) A method for treating or preventing the development of a cardiovascular disease in a subject comprising the steps of: detecting one or more alleles selected from the group

consisting of: allele 4 of the 222/223 marker of IL-1A, allele 4 of the gz5/gz6 marker of IL-1A, allele 1 of the -889 marker of IL-1A, allele 1 of the +3954 marker of IL-1B, allele 2 of the -511 marker of IL-1B, allele 3 of the gaat.p33330 marker, allele 3 of the Y31 marker, allele 2 of +2018 of IL-1RN, allele 1 of +4845 of IL-1A, allele 3 of the 222/223 marker of IL-1A, allele 3 of the gz5/gz6 marker of IL-1A, allele 2 of the -889 marker of IL-1A, allele 2 of the +3954 marker of IL-1B, allele 1 of the -511 marker of IL-1B, allele 4 of the gaat.p33330 marker, allele 6 of the Y31 marker, allele 1 of +2018 of IL-1RN, allele 2 of +4845 of IL-1A, and allele 1 of the VNTR marker of IL-1RN; and administering to the subject a therapeutic that compensates for a causative mutation that is in linkage disequilibrium with the IL-1 inflammatory haplotype.

66. (New) A method for treating or preventing the development of osteoporosis in a subject comprising the steps of: detecting one or more alleles selected from the group consisting of: allele 4 of the 222/223 marker of IL-1A, allele 4 of the gz5/gz6 marker of IL-1A, allele 1 of the -889 marker of IL-1A, allele 1 of the +3954 marker of IL-1B, allele 2 of the -511 marker of IL-1B, allele 3 of the gaat.p33330 marker, allele 3 of the Y31 marker, allele 2 of +2018 of IL-1RN, allele 1 of +4845 of IL-1A, allele 3 of the 222/223 marker of IL-1A, allele 3 of the gz5/gz6 marker of IL-1A, allele 2 of the -889 marker of IL-1A, allele 2 of the +3954 marker of IL-1B, allele 1 of the -511 marker of IL-1B, allele 4 of the gaat.p33330 marker, allele 6 of the Y31 marker, allele 1 of +2018 of IL-1RN, allele 2 of +4845 of IL-1A, and allele 1 of the VNTR marker of IL-1RN; and administering to the subject a therapeutic that compensates for a causative mutation that is in linkage disequilibrium with the IL-1 inflammatory haplotype.